APPENDIX A

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AF106851
LOCUS       AF106851                2816 bp    DNA     linear   BCT 08-APR-1999
DEFINITION  Staphylococcus aureus LytN (lytN) and FmhC (fmhC) genes, complete
            cds.
ACCESSION   AF106851
VERSION     AF106851.1  GI:4574236
KEYWORDS    .
SOURCE      Staphylococcus aureus
  ORGANISM  Staphylococcus aureus
            Bacteria; Firmicutes; Bacillales; Staphylococcus.
REFERENCE   1  (bases 1 to 2816)
  AUTHORS   Tschierske,M., Mori,C., Rohrer,S., Ehlert,K., Shaw,K.J. and
            Berger-Bachi,B.
  TITLE     Identification of three additional femAB-like open reading frames
            in Staphylococcus aureus
  JOURNAL   FEMS Microbiol. Lett. 171 (2), 97-102 (1999)
  MEDLINE   99177558
   PUBMED   10077832
REFERENCE   2  (bases 1 to 2816)
  AUTHORS   Shaw,K.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-1998) Chemotherapy and Molecular Genetics,
            Schering-Plough Research Institute, 2015 Galloping Hill Road 4700,
            Kenilworth, NJ 07033, USA
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="ATCC55748"
                     /db_xref="ATCC:55748"
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                     /gene="lytN"
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                     VPMTPLVEPKPKTVSSNNKSNSNSSTLNYLKTLENRGWDFDGSYGWQCFDLVNVYWNH
                     LYGHGLKGYGAKDIPYANNFNSEAKIYHNTPTFKAEPGDLVVFSGRFGGGYGHTAIVL
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     CDS             1372. .2616
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                     proteins"
                     /codon_start=1
                     /transl_table=11
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                     KNDKNEVIAACLLTEARIFKFYKYFYSHRGPLLDYFDAKLVCYFFKELSKFIYKNRGV
                     FILVDPYLIENLRDANGRIIKNYNNSVIVKMLGKIGYLHQGYTTGYSNKSQIRWISVL
                     DLKDKDENQLLKEMEYQTRRNIKKTIEIGVKVEDLSIEETNRFYKLFQMAEEKHGFHF
                     MNEDYFKRMQEIYKDKAMLKIACINLNEYQDKLKIQLLKIENEMMTVNRALNENPNSK
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RNKSKLNQLNMQLSSINNRISKTEELILEDGPVLDLAAALFICTDDEVYYLSSGSNPK
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ORIGIN

Alignment Scores:

Pred. No.:	1.1e-147	Length:	2816
Score:	2176.00	Matches:	414
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

US-09-932-474-1 (1-414) x AF106851 (1-2816)

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Qy         21 HisTyrThrGlnSerIleGluLeuTyrAsnTyrArgAsnLysIleAsnHisGluAlaHis 40
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Qy         41 IleValGlyValLysAsnAspLysAsnGluValIleAlaAlaCysLeuLeuThrGluAla 60
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Qy         61 ArgIlePheLysPheTyrLysTyrPheTyrSerHisArgGlyProLeuLeuAspTyrPhe 80
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Qy        141 HisGlnGlyTyrThrThrGlyTyrSerAsnLysSerGlnIleArgTrpIleSerValLeu 160
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Qy        161 AspLeuLysAspLysAspGluAsnGlnLeuLeuLysGluMetGluTyrGlnThrArgArg 180
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Qy        181 AsnIleLysLysThrIleGluIleGlyValLysValGluAspLeuSerIleGluGluThr 200
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Qy        201 AsnArgPheTyrLysLeuPheGlnMetAlaGluGluLysHisGlyPheHisPheMetAsn 220
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Qy        221 GluAspTyrPheLysArgMetGlnGluIleTyrLysAspLysAlaMetLeuLysIleAla 240
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Db       2032 GAAGATTATTTTAAACGAATGCAAGAAATATATAAAGATAAGGCAATGTTAAAGATAGCT 2091

Qy        241 CysIleAsnLeuAsnGluTyrGlnAspLysLeuLysIleGlnLeuLeuLysIleGluAsn 260
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Qy        261 GluMetMetThrValAsnArgAlaLeuAsnGluAsnProAsnSerLysArgAsnLysSer 280
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Qy        281 LysLeuAsnGlnLeuAsnMetGlnLeuSerSerIleAsnAsnArgIleSerLysThrGlu 300
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Qy        301 GluLeuIleLeuGluAspGlyProValLeuAspLeuAlaAlaAlaLeuPheIleCysThr 320
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Qy        321 AspAspGluValTyrTyrLeuSerSerGlySerAsnProLysTyrAsnGlnTyrMetGly 340
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Qy        341 AlaTyrHisLeuGlnTrpHisMetIleLysTyrAlaLysSerHisAsnIleAsnArgTyr 360
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Db       2392 GCATATCATCTACAATGGCATATGATAAAATATGCAAAATCACATAATATTAATAGGTAT 2451

Qy        361 AsnPheTyrGlyIleThrGlyValPheSerAsnGluAlaAspAspPheGlyValGlnGln 380
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Db       2452 AATTTTTATGGAATAACAGGCGTCTTTAGTAATGAGGCGGATGATTTTGGTGTTCAACAA 2511

Qy        381 PheLysLysGlyPheAsnAlaHisValGluGluLeuIleGlyAspPheIleLysProVal 400
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Qy        401 ArgProIleLeuTyrLysPheAlaLysLeuIleTyrLysVal 414
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APPENDIX B

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ID   Q9S685      PRELIMINARY;      PRT;   414 AA.
AC   Q9S685;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   FmhC.
GN   FMHC.
OS   Staphylococcus aureus.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC55748;
RX   MEDLINE=99177558; PubMed=10077832;
RA   Tschierske M., Mori C., Rohrer S., Ehlert K., Shaw K.J.,
RA   Berger-Bachi B.;
RT   "Identification of three additional femAB-like open reading frames in
RT   Staphylococcus aureus.";
RL   FEMS Microbiol. Lett. 171:97-102(1999).
DR   EMBL; AF106851; AAD23963.1; -.
DR   GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR   InterPro; IPR003447; Meth_resist.
DR   Pfam; PF02388; FemAB; 1.
SQ   SEQUENCE   414 AA;  49110 MW;  336D9BA80541E260 CRC64;

  Query Match             100.0%;  Score 2176;  DB 2;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-119;
  Matches  414;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 RIFKFYKYFYSHRGPLLDYFDAKLVCYFFKELSKFIYKNRGVFILVDPYLIENLRDANGR 120
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Qy        121 IIKNYNNSVIVKMLGKIGYLHQGYTTGYSNKSQIRWISVLDLKDKDENQLLKEMEYQTRR 180
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Qy        181 NIKKTIEIGVKVEDLSIEETNRFYKLFQMAEEKHGFHFMNEDYFKRMQEIYKDKAMLKIA 240
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Qy        241 CINLNEYQDKLKIQLLKIENEMMTVNRALNENPNSKRNKSKLNQLNMQLSSINNRISKTE 300
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Db        241 CINLNEYQDKLKIQLLKIENEMMTVNRALNENPNSKRNKSKLNQLNMQLSSINNRISKTE 300

Qy        301 ELILEDGPVLDLAAALFICTDDEVYYLSSGSNPKYNQYMGAYHLQWHMIKYAKSHNINRY 360
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Qy        361 NFYGITGVFSNEADDFGVQQFKKGFNAHVEELIGDFIKPVRPILYKFAKLIYKV 414
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Db        361 NFYGITGVFSNEADDFGVQQFKKGFNAHVEELIGDFIKPVRPILYKFAKLIYKV 414
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